ゲノムから解き明かすグリーランド氷床底部の古環境推定

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Reconstructions of past flora using DNA analysis from Greenland icecore samples

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Analyses of ice cores have often been used as a means to reconstruct past environments. The species composition of the organism such as microorganism and plant in the ice cores could reflect the environmental condition at that time. Thus, organisms in ice cores could be useful to reconstruct past environments. However, analysis of the biological contents in ice cores is still highly limited. We present results of metagenomic analyses of the Dye3 icecore sample taken in Greenland. The ice core samples were melted using a device that enabled us to obtain water only from the inner portion of the cores. Complete separation of the inner and outer cores is required to avoid contamination by bacteria that can adhere to the cores during drilling and storage. By sequencing the metagenomic DNA sampled in Greenland, we carried out phylogenetic and functional binning of the DNA sequences. We have detected more than 200 distinct species. Although a great majority of the detected species are of bacteria, we also found DNA sequences of archaea, fungi and a few animals and insects. Base on the detected species and functions of the genes, we attempted to reconstruct the ancient environment of the sampled site on Greenland. The results implied genomic information used as an environmental marker for past environmental analysis.